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<u>L3</u>	L2 same (advantag\$ or useful\$)	0	<u>L3</u>
<u>L2</u>	L1 same (candida near0 albicans)	16	<u>L2</u>
<u>L1</u>	ribosomal near0 RNA	2585	<u>L1</u>

END OF SEARCH HISTORY

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FILE 'CAPLUS' ENTERED AT 11:40:33 ON 23 DEC 2002
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=> s GroupI (w)intron(w)self(w)splicing
L1 0 GROUPI (W) INTRON(W) SELF(W) SPLICING

=> s GroupI (w)intron
L2 4 GROUPI (W) INTRON

=> s l2 (p)self (p)splicing
L3 0 L2 (P) SELF (P) SPLICING

=> s l2 (p)pneumocystis
L4 0 L2 (P) PNEUMOCYSTIS

=> s Group (w)I(w)intron
L5 2145 GROUP (W) I(W) INTRON

=> s l5 (p)(self(w)splicing)
L6 655 L5 (P)(SELF(W) SPLICING)

=> s l6 (p)pneumocystis
L7 43 L6 (P) PNEUMOCYSTIS

=> s l7(p)(candida(w)albicans)
L8 3 L7(P)(CANDIDA(W) ALBICANS)

=> duplicate remove
ENTER L# LIST OR (END):duplicate removeend
DUPLICATE IS NOT VALID HERE
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=> duplicate remove l8
DUPLICATE PREFERENCE IS 'BIOSIS, CAPLUS'
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PROCESSING COMPLETED FOR L8
L9 2 DUPLICATE REMOVE L8 (1 DUPLICATE REMOVED)

=> d his

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FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE' ENTERED AT 11:40:33 ON 23 DEC 2002

L1 0 S GROUPI (W) INTRON(W) SELF(W) SPLICING
L2 4 S GROUPI (W) INTRON
L3 0 S L2 (P) SELF (P) SPLICING
L4 0 S L2 (P) PNEUMOCYSTIS
L5 2145 S GROUP (W) I(W) INTRON
L6 655 S L5 (P) (SELF(W) SPLICING)
L7 43 S L6 (P) PNEUMOCYSTIS
L8 3 S L7(P) (CANDIDA(W) ALBICANS)
L9 2 DUPLICATE REMOVE L8 (1 DUPLICATE REMOVED)

=>

NT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000055374	A1	20000921	WO 2000-US7045	20000315
	W:	AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
	RW:	GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			

PRAI US 1999-124451P P 19990315

AB A method of inhibiting the **self-splicing** of a **Group I intron** is disclosed. The method uses an oligonucleotide having a sequence essentially identical to a guide sequence found in the 5' flanking exon and terminates with a 3' ribonucleoside. Usually the oligonucleotide has N3'.fwdarw.P5' phosphoramidate or thiophosphoramidate linkages rather than phosphodiester linkages. A method of inhibiting the growth of organisms having **Group I intron**, particularly certain pathogenic fungi including **Pneumocystis carinii**, **Candida albicans** and *Aspergillus nidulans* using the oligonucleotide is also provided.

RE.CNT 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 2 OF 2 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 1
AN 1996:274285 BIOSIS
DN PREV199698830414

TI Group I introns in 26S rRNA genes of *Gaeumannomyces graminis* as possible indicators of host specificity of *G. graminis* varieties.

AU Tan, M. K.; Wong, P. T. W.

CS Biol. Chem. Res. Inst., NSW Agric., PMB 10, Rydalmere, NSW 2116 Australia

SO Mycological Research, (1996) Vol. 100, No. 3, pp. 337-342.

ISSN: 0953-7562.

DT Article

LA English

AB The 26S rRNA genes of *Gaeumannomyces graminis* exhibit length polymorphisms due to the presence of introns. Three group I introns have been discovered and their distribution appears to correlate with the three varieties of *G. graminis*. No intron is found in var. *graminis* and *Phialophora* sp. (lobed hyphopodia) which are generally not pathogenic to wheat, oats and barley. *G.g.* var. *avenae* isolate, 91/56 and var. *tritici* isolate, 90/921 have a common intron (intron AT) and a unique intron each (intron A and intron T respectively). The three introns are inserted at different sites in the 26S rRNA genes. Intron T is **self-splicing**. The sequence of intron A is more similar to the intron I of the 26S rRNA gene from human-derived **Pneumocystis carinii** isolate, Pc3 and of the 18S rRNA of *Ustilago maydis* than to the other two *G. graminis* group I introns. The catalytic core elements and stem P8 of intron T are extremely similar to corresponding regions of the **group I intron** in the 26S rRNA gene of **Candida albicans**. Intron AT has a unique sequence. Each of the three introns appeared to have a different origin.

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